



0200  
0400

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/005,337

Source: 01PE

Date Processed by STIC: 12/14/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 101005337

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos    was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                          prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering               use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                          ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                          each n or Xaa can only represent a single residue. Please present the maximum number of each  
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                   sequences(s)     . Normally, PatentIn would automatically generate this section from the  
                          previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                          the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                          Artificial or Unknown sequences.
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response               scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                          is Artificial Sequence
  
- 11 ✓ Use of <220>            Sequence(s) 4+5 missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                          "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                          listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIFE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,337

DATE: 12/14/2001

TIME: 09:51:23

Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: BENOIT, Patrick  
 4 SCHWARTZ, Bertrand  
 5 BRANELLEC, Didier  
 6 CHIEN, Kenneth R.  
 8 <120> TITLE OF INVENTION: SEQUENCES UPSTREAM OF THE CARP GENE, VECTORS CONTAINING  
 9 THEM AND USES THEREOF  
 11 <130> FILE REFERENCE: 03806.0530-00000  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/005,337  
 15 <141> CURRENT FILING DATE: 2001-12-07  
 17 <160> NUMBER OF SEQ ID NOS: 5  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2358  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Mus musculus  
 26 <400> SEQUENCE: 1  
 27 ggatocctttc atgtttaaca atatcaaccc taacccaagg ggaacagcct gcctgacagt 60  
 28 ggcttttgcca cccatgaata ctctcctagtc tagtccggtt gtgaaactca gcccacccca 120  
 29 acaattctgc aagccccatc ctctacaagg tgctcattgg gaatttcctg gagcttctct 180  
 30 ttcaggatca gcctgattct agggcagcag ttctcaacct gggggcctcg accccttttg 240  
 31 gggaatcaaa cgacccttta caggggtcac atatcatcta tcctatatgt cagggtattta 300  
 32 cattacgatt cgtaacagta gcaaaattac aggtatgaaa tagcaatgaa ataattttat 360  
 33 gattgaagggt caccacaaca tgaggccggc acactgttct agagaaaaat cacctgggtg 420  
 34 gggaaagggt tgggaaagcc tttctgtcca ttcttcattc ttcaaagtga tgtgttcaca 480  
 35 gaaagccttt cagctgttct gctggggctc ttagtaagtc tgagtaggaa ctgtatgtac 540  
 36 cagggtctgct tcttatgggt ggagccaaga cgcctcgtgg gtggagcgaa gacgcaacct 600  
 37 caccttctag ctctgcatcc atagcaagta gcctaattgt tctgtgtcta ggtgtcatct 660  
 38 ctgtgaatcg agatccttgg ccttgcttga attagggagg cacaaaatac tcagagattc 720  
 39 aagactgctc agcagcccag agtcttctc caaaggaaag gtctcaactc tcagcccccc 780  
 40 ttagctctga gtcaggcctg gaacaaacgg ccacaggaat gagaaaagct gccatagctg 840  
 41 cttgtcactt caagaggtea aagaaaatag tgttaaccat gaaaacgaga agaccaacag 900  
 42 ttatccattg atagcgtctc aggacagata ggacagagag aacactagga gaggggaacc 960  
 43 cacgaaggac aaggtattag tgtgttggtt ttcagggcaa tgtcttgtag tgaagattct 1020  
 44 agaaacacaa tttgctgggt gaacagctga agtgggggtg gggttcttac cccatgttca 1080  
 45 tggaagggtg agtgaggaga gacagatata tgatggccag cataacaaac atacacaaca 1140  
 46 ccctaattaa cacttccctc ttctactgac acccccttca ctctcctctt tcataaaaaa 1200  
 47 taaaaaaagt attttatgtg gctcttacga tagaatcttt cctcgaacta taaaaagatc 1260  
 48 taaatattta tatttttcac attttaatat cttagcgatg acaagccaga aacaagtatt 1320  
 49 ttttgctctc ctcaacagca aagcttgggg cctttttggt tccgtgttag gaatagaaca 1380  
 50 cgagagcccc gtgtatctag gcagatgctc tatcatagc ccatgagtct ccagcctcag 1440  
 51 acgcacattt ttctcgggct ctcttaagct ttcccacag cattgggaaa ctttactgac 1500  
 52 agcatccaag ttgtgcttct gctaagaact ggactcacat ctctctgtgc atcacttcgg 1560  
 53 cccgttttgg ggtagatcct ctgattagcc ttcagattta gaacacggtg agcctgtgg 1620  
 54 gcaactaatta tggccagtga caccatagag tcaaagtgca ttactgaatg ctttcaattt 1680  
 55 ctctaatgct tggtagcatg gcatgtcaca gggccatttt agctgcagac atcactccag 1740  
 56 agaattccaa acagatagag acaagtggca cccagaccca tctccttccc ctcggtctga 1800  
 57 ttatccccag aaataggatg tcccaaagca acacttccca gccaaactgga gtgctgataa 1860

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,337

DATE: 12/14/2001

TIME: 09:51:23

Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

```

58 gtccagttat cagaaagata tggctgtaag tgtgatgcac agtgcttgca ttttcttgat 1920
59 acgttagtca tatgagagct gacaaagaag gaaaaagagc agcgatgtgg tgcaatatta 1980
60 acaggcagct gtcccttggc ttcccgatac gtgggatgac tcgcattgct gagcgggtgtg 2040
61 gtcactgcca aaggaatgac cctctcacat ttcttctga ttgcatacg ccgcggccag 2100
62 ctgtcatct cctcttggg cttccagac actaagtctg gaatgaaat tcacctgcct 2160
63 ctgaattggc cactggtggg ggcaggggtg tgacttggct tcccaggctg gaagattatc 2220
64 tcaccagcc ctactatat aacgggctgg tgtggagggg ctccacaggg ccagttccag 2280
65 gggttcatcc acaagagaga aaaacataga ctcgaggtct agggagcttg catgcctgca 2340
66 ggtcggaggc caccatgg                                     2358
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 2074
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 2
75 ctgcagcaag ttacttaatg ttttttgct cagcatcctc tctgtaaaat gagagcatta 60
76 gtcttgctcc aacttcgagg gcatggacag ctctgggatt tcatatccaa gacccttaa 120
77 catccacag tccttcccc aaacacttct cctcctaata cctccctcag tttgggtcag 180
78 gcctggaaca aaaaggcata cgaaatggta gaaaaagtgt ccatgactac ttctgactta 240
79 gatgaagaga ccaatgaaaa tagtaatgac tctgtttgct tcagcaggac atatactaaa 300
80 ataggagcta tacaagaag attagcatgg actctgtgca agaatgacac acaaatttgt 360
81 gaaacattcc atatatataa aataaataaa taataaagag aaaaggaaaa aattaaaaag 420
82 aaaatagtga tagctgtgtc catctcaaag aaaagcccag gagatttctt ttatttacc 480
83 cctttaagat agaattatag gagaccggaa catatgatac aggaggtact gggagggtcc 540
84 ctctttgtca atgtttgtc ttgggggtgg gagtcgatgt ctctcaaag tttcagaaac 600
85 accatccact gactgagcat tcaaggggca agaggagaat ggcagccaca tttgttgatt 660
86 ggggtgagttt ggggagaaat agacacacaa aggtcaaaca taacttccta attaacactt 720
87 cctccattc acaattccct tctccattc ttctctctctg tcttttacts akaraaacc 780
88 agtttttctt gaaactataa aaataccccc agtatgttta cataatttac acctcaaaga 840
89 ttagaaacca gaaatagaga ctttttcaac ccttcgggaa gcaaagtgca ttatccctcc 900
90 agccacgtgt ctcaaattct gatgcacag aatcatctgg gtgctttkaa attcaagatg 960
91 attctacga gttaccataa atcaactcag aattccctgg agtggggcca gggatctgta 1020
92 tttctgacaa gctcccacag gtgattcctt tcccacagc atttgagaac ttcagctcaa 1080
93 tgacctaatc agagtcctgc cattgctaatt atctggtctc atttttbtca tatatatata 1140
94 tagtatttgt ggtagagatg ggattttgcc atgttgccca ggctagtatt gaactcctaa 1200
95 gctaagcaat ctctctgtct ctgcctccca aaatgttggg attacagggt taagccactg 1260
96 caccggctg atagctggtt tcatttactc ttttcttga ccactctgat ccattttgaa 1320
97 gtaaaaatgc tccaattatt atgctgtttt agaacacggg aagcatgtca tgtgctaatt 1380
98 gccagtgaca tcataaaaga aaagtgcatt actgaatgct ttcaatgtct tataatgatg 1440
99 gtaaggtggc atgtcatggg gcctatttag ccagacatc actccaaaga attccaaaca 1500
100 gatatagaca agtgccctta gggcccagat cccttccct caggctgttt acccaggga 1560
101 taggatgtcc tgggacaagt ttcccctaag tgaagtgttg ataagtctgc ttatcagaaa 1620
102 gatattactg ggggtgtgat atgtagggca tctacatttt ctgatagggt agtcatatga 1680
103 aagctgacaa agaaaaaaag ggcagtgatg tggtgcaatg tcaacagaca gctgtccct 1740
104 gactcttgac aaataggatg acttgcatg ctgagcgatg tgatcaccac caaaggaaatg 1800
105 gccctctcac atttcttctt gattcacata ttcagcaggg ttagcttgtc ctccctccc 1860
106 tcttcagctt cccagacact gagtctggaa tgaaaattca cctgcctctg agttggctcc 1920
107 taatgggggc gggagtgtta cttcggttcc caggttgga gattatctca cccggcccca 1980
108 gctatataag ctgaccgggt tggaggggcc cagcagggcc aactccaggg attccttcca 2040
109 cgacagaaaa acatacaaga ctcttcagc caac                                     2074

```

## RAW SEQUENCE LISTING

DATE: 12/14/2001

PATENT APPLICATION: US/10/005,337

TIME: 09:51:23

Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

```

112 <210> SEQ ID NO: 3
113 <211> LENGTH: 750
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 3
118 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
119   1           5           10           15
121 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
122           20           25           30
124 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
125           35           40           45
127 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
128           50           55           60
130 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
131           65           70           75           80
133 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
134           85           90           95
136 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
137           100          105          110
139 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
140           115          120          125
142 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
143           130          135          140
145 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
146           145          150          155          160
148 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
149           165          170          175
151 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
152           180          185          190
154 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
155           195          200          205
157 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
158           210          215          220
160 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
161           225          230          235          240
163 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
164           245          250          255
166 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
167           260          265          270
169 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
170           275          280          285
172 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
173           290          295          300
175 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
176           305          310          315          320
178 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
179           325          330          335
181 Leu Asp Leu Asn Asp Gln Val Thr Leu Lys Tyr Gly Val His Glu
182           340          345          350

```

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Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

```

184 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
185           355           360           365
187 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
188           370           375           380
190 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
191 385           390           395           400
193 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
194           405           410           415
196 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
197           420           425           430
199 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
200           435           440           445
202 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
203           450           455           460
205 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
206 465           470           475           480
208 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
209           485           490           495
211 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr Ala Trp Ala Ile Leu Thr Gly
212           500           505           510
214 Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu
215           515           520           525
217 Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln
218           530           535           540
220 Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe
221 545           550           555           560
223 Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile
224           565           570           575
226 Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys
227           580           585           590
229 Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn
230           595           600           605
232 Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu
233           610           615           620
235 Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys
236 625           630           635           640
238 Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp
239           645           650           655
241 Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly
242           660           665           670
244 Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln
245           675           680           685
247 Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu
248           690           695           700
250 Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr
251 705           710           715           720
253 Glu His Val Gln Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
254           725           730           735
256 Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr

```

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Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

257                      740                      745                      750

260 <210> SEQ ID NO: 4

261 <211> LENGTH: 30

262 <212> TYPE: DNA

263 <213> ORGANISM: Artificial sequence

W--> 265 <220> FEATURE:

W--> 265 <223> OTHER INFORMATION:

265 <400> SEQUENCE: 4

C--> 266 ggcgatttaa ataatgtagt cttatgcaat 30

269 <210> SEQ ID NO: 5

270 <211> LENGTH: 31

271 <212> TYPE: DNA

272 <213> ORGANISM: Artificial sequence

W--> 274 <220> FEATURE:

W--> 274 <223> OTHER INFORMATION:

274 <400> SEQUENCE: 5

C--> 275 ggggtctaga aggtgcacac caatgtggtg a 31

Requires 2207 to 2233 - with explanation  
for Artificial sequence; see error  
summary sheet item 11

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/005,337

DATE: 12/14/2001

TIME: 09:51:24

Input Set : A:\Seqlist6064.txt

Output Set: N:\CRF3\12142001\I005337.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:265 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:265 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:266 M:112 C: (48) String data converted to lower case,  
L:274 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:274 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:275 M:112 C: (48) String data converted to lower case,